

Station	Time	Lat	Long	Alt	Temp	Hum	Wind	Dir	Speed	Pressure	Clouds	Vis	Remarks
117235	0800	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117240	0815	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117245	0830	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117250	0845	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117255	0900	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117300	0915	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117305	0930	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117310	0945	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117315	1000	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117320	1015	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117325	1030	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117330	1045	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117335	1100	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117340	1115	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117345	1130	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117350	1145	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117355	1200	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117400	1215	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117405	1230	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117410	1245	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117415	1300	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117420	1315	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117425	1330	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117430	1345	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117435	1400	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117440	1415	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117445	1430	33° 15' N	117° 15' W	10	18.5	85	10	090	10	1010.5	0	10	Light rain
117450	1445	33° 15' N	117° 15' W	10	18.5	85	10						

FIG. 1

ATGACGTCCACCTGCACCAACAGCACGCGCAGAGTAACAGCAGCCACACGTGCATGCCCTCTCCAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGGTTATCTTCTCGCCGCCTCTTTTCGTGGCAACATAGTGCTGGCGCTAGTGTTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTTATCTTTAACTCCTCGTCACCGACCTGCTGCAGATTTTCGTTCGTGGCCCCCTGGGTGGTGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAAGCCACTTTGCACGGCCCTGGTTAGCCTCACCCACTGTTGCCTTCGCCCATCGCAGCTCAACACCATTTGTCTTGGTGTGCAGTGGATCGCTACTTTGTCCATCATCCACCCCTCTCTCCTACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACCTGGATTGTGGCCATCTGTCAGAGCACTCCTCCACTCTACGGCTGGGGCCAGGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCAGCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCTATCGTCATTCCACTGATTGTCTATGATTGCCTGCTACTCCGTGGTGTCTGTGTCAGCCCGGAGGCAGCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCGAGTCAAGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAGTTCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGCCAAGGAGGGCAGAATGGAAGCCAGCAGCGCAGCCTGAAGGCCAAGGAAGGAAGCAGCGGGACAGTGAAGTAGTGTAGAGGCCAGGGGCAGCGAGGAGGTGAGAGAGAGCAGCACGGTGGCCAGCGCAGCGCAGCATGGAGGGTAAGGAAGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTTCGCACAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTTGGTGAAGACGACATCAATTTCAAGTGAAGGATGACGTCGAGGCAGTGAACATCCCGGAGAGCCTCCCACCCAGTTCGTGTAACAGCAACAGCAACCCTCCTCTGCCCAGGTGCTACCAGTGCAAAGCTGCTAAAGTGATCTTCATCATCATTTTTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTCTGGCCGTGTGGGTGGATGTGCAAACCCAGGTACCCCAAGTGGGTGATCACCATAATCATCTGGCTTTTCTTCTTCAGTGTGCTATCCACCCCTATGTCTATGGCTACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTTCTTCTGCAAGGAAAAGCCCCGAAAGAAATAGCCACCCAGACCTGCCCGAAGCAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCTACTTTTCTTTGA

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FIG.2

MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
QLLQVTNRFI FNLLVTDLLQISLVAPWVSVPLFWPLNSHFCTALVSLTHLFAFASVN
TIVLVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
LCSMIWGASPSYTIILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
CVENEDEEGAEEKKEEFQDESEFRROHEGEVKAKEGRMEAKDGSCLKAKEGSTGTSESSVEA
RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
NFSEDDVEAVNIPESLPPSRNSNSNPPLPRCYQCKAAKVIFIIIFSIVLSLGPYCFILAV
LAVWVDVETQVPQWVITIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK
EDSHPDLPGTEGGTEGKIVPSYDSATFP

FIG. 3

GCAACCTGTCTCACGCCCTCTGGCTGTTGCC

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FIG. 4

AGTTAGTTCTAAGGCAAACCTT

FIG. 5

1	MTSTCTNSTR	ESNSSHTCMP	LSKMPISLAH	GIIRSTVLVI	<u>FLAASFVGNI</u>
51	<u>VLALVLQ</u> RKP	QLLQVTNRFI	<u>FNLLVTDLLQ</u>	<u>ISLVAPWVVA</u>	<u>TSVPLEFWPLN</u>
101	<u>SHFCTALVSL</u>	<u>THLFAFASVN</u>	<u>TIVLVSVDRY</u>	LSIIHPLSYP	SKMTQRRGYL
151	<u>LLYGTWIVAI</u>	<u>LQSTPPLYGW</u>	GQAAFDERNA	LCSMIWGASP	SYTILSVVSF
201	<u>IVIPLIVMIA</u>	<u>CYSVVFCAAR</u>	RQHALLYNVK	RHSLEVRVKD	CVENEDEEGA
251	EKKEEFQDES	EFRRQHEGEV	KAKEGRMEAK	DGSLKAKEGS	TGTSESSVEA
301	RGSEEVRESS	TVASDGSMEG	KEGSTKVEEN	SMKADKGRTE	VNQCSIDLGE
351	DDMEFGEDDI	NFSEDDVEAV	NIPESLPPSR	RNSNSNPPLP	RCYQCKAAKV
401	<u>IFIIIFS</u> YVL	<u>SLGPYCFLAV</u>	LAVWVDVETQ	VPQWVITIII	<u>WLEFLQCCIH</u>
451	<u>PYVYGYMHKT</u>	IKKEIQDMLK	KFFCKEKPPK	EDSHPDLPGT	EGGTEGKIVP
501	SYDSATFP				

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FIG. 6A

ACM4_CHICK	~~~~~
YDBM_CAEEL	~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~MANFTFGDLALDVARMGGLASTPSGLRSTGLTTPGLSPT
A1AD_HUMAN	MTFRDLLSVSFEGPRPDSSAGGSSAGGGGGSAGGAAPSEG
A1AD_MOUSE	MTFRDILSVTFEGPRASSSTGGSGAGGGAGTVG...P.EG
Q13675	~~~~~
Q13729	~~~~~
O60451	~~~~~
A1AA_RAT	~~~~~
O54913	~~~~~
A1AA_BOVIN	~~~~~
A1AA_CANFA	~~~~~
A1AA_RABIT	~~~~~
A1AA_HUMAN	~~~~~
A1AA_ORYLA	~~~~~
O96716	~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~
ACM4_CHICK	~~~~~MHNLSAQPWQAKMANITYDNVTLSN
YDBM_CAEEL	MCFAEKGEAGEDVDHHS LFC.P.KKLVGNL...KGFIRN
5H1A_HUMAN	~~~~~MDV..LSPGQ...GNNTT...SPPAPFETGGN
5H1A_MOUSE	~~~~~MDM..FSLGQ...GNNTT...TSLEPFGTGGN
5H1A_FUGRU	~~~~~MDLRATSSND...SNATSGYSDTAAVDWDEGEN
5HT_LYMST	GLVTSDFNDSYGLT.GQFINGSHSSRSRDNASANDTSATN
A1AD_HUMAN	PAVGGVPGGAGGGGGVVGAGSGEDNRSSAGEPGSAGAGGD
A1AD_MOUSE	PAVGGVP.GATGGS AVVGTGSGEDNQSS TAEAGAA.ASGE
Q13675	~~~~~MVFLSGNASDS
Q13729	~~~~~MVFLSGNASDS
O60451	~~~~~MVFLSGNASDS
A1AA_RAT	~~~~~MVLLSENASEG
O54913	~~~~~MVLLSENASEG
A1AA_BOVIN	~~~~~MVFLSGNASDS
A1AA_CANFA	~~~~~MVFLSGNASDS
A1AA_RABIT	~~~~~MVFLSGNASDS
A1AA_HUMAN	~~~~~MVFLSGNASDS
A1AA_ORYLA	~~~~~MTPSSVTLNC
O96716	~~~~~MSANTTVSPTETTANLTANSTEA
O75963	~~~~~MSLNSSL
HGPRBMY8	~~~~~MTSTCTNSTRESNS

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FIG. 6B

ACM4_CHICK
YDBM_CAEEL
5H1A_HUMAN
5H1A_MOUSE
5H1A_FUGRU
5HT_LYMST
A1AD_HUMAN
A1AD_MOUSE
Q13675
Q13729
O60451
A1AA_RAT
O54913
A1AA_BOVIN
A1AA_CANFA
A1AA_RABIT
A1AA_HUMAN
A1AA_ORYLA
O96716
O75963
HGPRBMY8

RSEVAIQPTNYKTVELVFIATVTGSLS..LVTVVGNILV
QYH.....QHETIQ..ILKGSALFLLV..LWTIFANSLV
ITG...ISDVTVSQ..VITSLLLGTLI..FCAVLGNACV
DTG...LSNVTFVSQ..VITSLLLGTLI..FCAVLGNACV
ATGSGSLDPETVSQ..IITSIFLGALI..LCSTFGNSCV
MTDDRYWSLTVYSHEHLVLTSVILGLFV..LCCITGNCV
V.NGTAAVGGLVSAQGVGVFLAAFI..LMAVAGNLLV
V.NGSAAVGGLVSAQGVGVFLAAFI..LTAVAGNLLV
S.NCTQPPAP.VNISKAILLGVLGGLI..LFGVLGNILV
S.NCTQPPAP.VNISKAILLGVLGGLI..LFGVLGNILV
S.NCTQPPAP.VNISKAILLGVLGGLI..LFGVLGNILV
S.NCTHPPAP.VNISKAILLGVLGGLI..IFGVLGNILV
S.NCTHPPAQ.VNISKAILLGVLGGLI..IFGVLGNILV
S.NCTHPPPP.VNISKAILLGVLGGLI..LFGVLGNILV
S.NCTHPPAP.VNISKAILLGVLGGLI..IFGVLGNILV
S.NCTHPPAP.VNISKAILLGVLGGLI..LFGVLGNILV
S.NCTQPPAP.VNISKAILLGVLGGLI..LFGVLGNILV
S.NCSHVLAPETNTVKAIVLGMVLGIFI..LFGVLGNILV
SVGSCFAPNPYSAGVQAV.LGLITVILI..LLTVIGNVLV
CRKELSNLTEEEGGEGGVITQFLAIVITIFVCLGNLVI
SHTCMPLSKMPISLAHGITRSTVL..VIFLAASEVGNIVL

ACM4_CHICK
YDBM_CAEEL
5H1A_HUMAN
5H1A_MOUSE
5H1A_FUGRU
5HT_LYMST
A1AD_HUMAN
A1AD_MOUSE
Q13675
Q13729
O60451
A1AA_RAT
O54913
A1AA_BOVIN
A1AA_CANFA
A1AA_RABIT
A1AA_HUMAN
A1AA_ORYLA
O96716
O75963
HGPRBMY8

MLSTKVNROLOIVNNYELFSLACADLIIGVFMSNLYTVYI
FIVLYKNPRLQIVPNLLVGNLAFSDIALGLIVLPSSVYA
VAATALERSLQNVANYLIGSLAVTDLMSVLVLPMAALYQ
VAATALERSLQNVANYLIGSLAVTDLMSVLVLPMAALYQ
VAATALERSLQNVANYLIGSLAVTDLMSVLVLPMAALYQ
IAAVMLERSLHNVANLYLISLAVADLMVAVLVMPLSVVS
ILSVACNRHLQIVTNYEIVNLAVADLLLSATVLPFSATME
ILSVACNRHLQIVTNYEIVNLAVADLLLSAAVLVLPFSATME
ILSVACHRHLSVTHYYIVNLAVADLLLTSTVLVLPFSATFE
ILSVACHRHLSVTHYYIVNLAVADLLLTSTVLVLPFSATFE
ILSVACHRHLSVTHYYIVNLAVADLLLTSTVLVLPFSATFE
ILSVACHRHLSVTHYYIVNLAVADLLLTSTVLVLPFSATFE
ILSVACHRHLSVTHYYIVNLAVADLLLTSTVLVLPFSATFE
ILSVACHRHLSVTHYYIVNLAVADLLLTSTVLVLPFSATFE
ILSVACHRHLSVTHYYIVNLAVADLLLTSTVLVLPFSATFE
ILSVACHRHLSVTHYYIVNLAVADLLLTSTVLVLPFSATFE
ILSVACHRHLSVTHYYIVNLAVADLLLTSTVLVLPFSATFE
ILSVACHRHLSVTHYYIVNLAVADLLLTSTVLVLPFSATFE
ILSVACHRHLSVTHYYIVNLAVADLLLTSTVLVLPFSATFE
ILAVTCHRKMRITVTNFIIVSLACADLSVGITVLPFAATND
VVTLYKKSILLISNKEVFSLTISNELLVSVLVLPFVVTSS
ALVLRKPOLLOVTNREIFNLLVTDLLQISLVAPVWVATS

Figure 1 is a schematic representation of the experimental design. It shows a flow from 'Study 1' to 'Study 2' and 'Study 3'. Study 1 involves 'Pretest' and 'Main Study'. Study 2 involves 'Pretest' and 'Main Study'. Study 3 involves 'Pretest' and 'Main Study'. The flow is indicated by arrows and labels like 'Study 1', 'Study 2', and 'Study 3'.

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FIG. 6D

ACM4_CHICK	QFIVGKRTVHE.....RECYIQFLSNPAVTFGTATAAFYL
YDBM_CAEEL	QTAQTPNLIYEKNNTVRQC..TFLDLPSYTVYSATGSFFI
5H1A_HUMAN	R.TP.EDRSDPDA.....CTIS..KDHGYTIYSTFGAFYL
5H1A_MOUSE	R.AP.EDRSNPNE.....CTIS..KDHGYTIYSTFGAFYL
5H1A_FUGRU	R.SA.EDRANPDA.....CIIS..QDPGYTIYSTFGAFYL
5HT_LYMST	R.DENNDPKTGT.....CIIS..QDKGYTIYSTFGAFYL
A1AD_HUMAN	K.EPVPP.....DERFCGIT..EEAGYAVFSSVCSFYI
A1AD_MOUSE	K.EPVPP.....DERFCGIT..EEVGYATFSSVCSFYI
Q13675	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYL
Q13729	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYL
O60451	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYL
A1AA_RAT	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYV
O54913	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYV
A1AA_BOVIN	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYV
A1AA_CANFA	R.QPAPE.....DETTTCQIT..EPPGYVLFSAIGSFYV
A1AA_RABIT	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYV
A1AA_HUMAN	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYL
A1AA_ORYLA	K.EPAPE.....DETVCKIT..EPPGYATFSAVGSFYI
O96716	R.DNQSEEALAIYSDPCLCIFT..ASTAYTTVSSLISFYI
O75963	S.VEFDEFKWM.....CVAAWH..REPGYTAFWQIWCALF
HGPRBMY8	QA.....AFDERNALCSMIWGASPSYTTLSVVSFIVI

ACM4_CHICK	PVVIMTVLYIHISLA.SRSRVRRHKPESRKERKGSLSFF
YDBM_CAEEL	PTLLMFFVYFKTIYQAFAKHRARQIYRQKVIRKHIESTILH
5H1A_HUMAN	PLLLMLVLYGRIFERA.....ARFRIRKTVKKVEK.....
5H1A_MOUSE	PLLLMLVLYGRIFERA.....ARFRIRKTVKKVEK.....
5H1A_FUGRU	PLILLMLVLYGRIFERKA.....ARFRIRKTVKKTEKA.....
5HT_LYMST	PMLVMMITTYIRIWLTV.....ARSRIKDKFQMTKARL...
A1AD_HUMAN	PMAMIVVMYCRVYVV.....A.....RSTTRSL...
A1AD_MOUSE	PMAMIVVMYCRVYVV.....A.....RSTTRSL...
Q13675	PLAIILVMYCRVYVV.....A.....KRESRGL...
Q13729	PLAIILVMYCRVYVV.....A.....KRESRGL...
O60451	PLAIILVMYCRVYVV.....A.....KRESRGL...
A1AA_RAT	PLAIILVMYCRVYVV.....A.....KRESRGL...
O54913	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_BOVIN	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_CANFA	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_RABIT	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_HUMAN	PLAIILVMYCRVYVV.....A.....KRESRGL...
A1AA_ORYLA	PLAIILVMYCRVYVV.....A.....OKESRGL...
O96716	PLLIIMLVFYGIIFERKA.....A.....RDQARKI...
O75963	PFLVMLVCYGFIERV.....ARV.....KARKV...
HGPRBMY8	PLIIVMIACYSVVECAARRQHA.LLYNVKRHSLEVRVKDCV

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FIG. 6E

ACM4_CHICK	KAPPVKQNNNN	SPKRAVEVKEEVRNGKVDDQPSAQTEATG
YDBM_CAEEL	EISHVLPTSDEFAKEEEEEEDSESSGQVENGLGNGNDAI.	
5H1A_HUMANTGADTRHGASPAQPK..KSVNG.....E..	
5H1A_MOUSEKGAGTSFGTSSAPPPK..KSLNG.....Q..	
5H1A_FUGRUKASDMCLTLSPAVFHK..RA.NG.....D..	
5HT_LYMSTKTEETTLVASPKTEYSVVSDCNGCNSPD..	
A1AD_HUMANEA.....GVKREER..	
A1AD_MOUSEEA.....GIKREP..	
Q13675KS.....GLKTDK..	
Q13729KS.....GLKTDK..	
O60451KS.....GLKTDK..	
A1AA_RATKS.....GLKTDK..	
O54913KS.....GLKTDK..	
A1AA_BOVINKS.....GLKTDK..	
A1AA_CANFAKS.....GLKTDK..	
A1AA_RABITKS.....GLKTDK..	
A1AA_HUMANKS.....GLKTDK..	
A1AA_ORYLAKE.....GOKIEK..	
O96716NA.....LEG..	
O75963HCGTVVIVEEDAQRTGRKNSSTSTS..SSG..	
HGPRBMY8	ENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDG	
ACM4_CHICK	QQEEKETS NESSTVSM TQTTKDKPTTEILPAGQGQSPAHP	
YDBM_CAEEL	.IEEDECEDEDSDEKRDDHTS...MTTVTATVTGPT EA.P	
5H1A_HUMAN	..SGSRNWRLGVESKAGGALCANGAVRQGDDGAAL.EVIE	
5H1A_MOUSE	..PGSGDCRRSAENRAVGTPCANGAVRQGEDDATL.EVIE	
5H1A_FUGRU	..AVSAEWKRGYKFKP..SSPCANGAVRHGEEMESL.EVIE	
5HT_LYMST	..STTEKKKRRAPFKSYG..CSPRPERKKNRAKKLPENAN	
A1AD_HUMAN	..GKAS.....EVVL	
A1AD_MOUSE	..GKAS.....EVVL	
Q13675	..SDSE.....QVTL	
Q13729	..SDSE.....QVTL	
O60451	..SDSE.....QVTL	
A1AA_RAT	..SDSE.....QVTL	
O54913	..SDSE.....QVTL	
A1AA_BOVIN	..SDSE.....QVTL	
A1AA_CANFA	..SDSE.....QVTL	
A1AA_RABIT	..SDSE.....QVTL	
A1AA_HUMAN	..SDSE.....QVTL	
A1AA_ORYLA	..SDSE.....QVIL	
O96716	
O75963	..SRRNAFQGVVYSANQCKALITILVVLGAFMVTWGPYM	
HGPRBMY8	SLKAKEGSTGTSESSVEARGSEEVRRESSTVASDGSMEGKE	

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FIG. 6F

ACM4_CHICK	RVNPTSKWSKIKIVTKQTGTESVTAIEIVPAKAGASDHNS
YDBM_CAEEL	YMKREAKISKSVPIEKESAIQKREAKPMRSVMAISYEKVK
5H1A_HUMAN	.VHRVGNSKEHLPL....PSEAGPT....PCAP....ASF
5H1A_MOUSE	.VHRVGNSKGDPL....PSESGAT....SYVP....ACL
5H1A_FUGRU	.VN..SNSKTHLPL....PN....T....P.QS....SSH
5HT_LYMST	GVNSNSSSSERLKQIQIETAEAFAN....GCAEEASTAML
A1AD_HUMAN	RIHC.....RGAAT....GADGAHGMRSA
A1AD_MOUSE	RIHC.....RGAAT....SAKGNPGTQSS
Q13675	RIHR.....KNAPA.....GSGMASA
Q13729	RIHR.....KNAPA.....GSGMASA
O60451	RIHR.....KNAPA.....GSGMASA
A1AA_RAT	RIHR.....KNVPA.....EGGGVSSA
O54913	RIHR.....KNVPA.....EGSGVSSA
A1AA_BOVIN	RIHR.....KNAQV.....GSGGVTS
A1AA_CANFA	RIHR.....KNAPV.....GGTGVSSA
A1AA_RABIT	RIHR.....KNAPA.....GSGGVASA
A1AA_HUMAN	RIHR.....KNAPA.....GSGMASA
A1AA_ORYLA	RMHR.....GNTTV.....SEDEAL
O96716	RLEQ.....EN.....NRGKKISLA
O75963	VI...ASEALWGKSSVSPSLETWAT....WLSFASAVCHP
HGPRBMY8	GSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDINF

ACM4_CHICK	LSNSRPANVARKFASTARSQVRKKROMAAR..EKKVTRTII
YDBM_CAEEL	RHKNRKERIYRK..SLQR...KPKAISAAK..ERRGVKVL
5H1A_HUMAN	ERK..NERN.....AEAKRKMA..LAR..ERKTVKTL
5H1A_MOUSE	ERK..NERT.....AEAKRKMA..LAR..ERKTVKTL
5H1A_FUGRU	ENI..NEKT.....TGTRRKIA..LAR..ERKTVKTL
5HT_LYMST	ERQCNNGKKISSNDIPYSRTREKLE..LKR..ERKAARTL
A1AD_HUMAN	KG.....HTFRSSLSV.....RLLK..FSR..EKKAAKTL
A1AD_MOUSE	KG.....HTLRSSLSV.....RLLK..FSR..EKKAAKTL
Q13675	KT.....KT...HFSV.....RLLK..FSR..EKKAAKTL
Q13729	KT.....KT...HFSV.....RLLK..FSR..EKKAAKTL
O60451	KT.....KT...HFSV.....RLLK..FSR..EKKAAKTL
A1AA_RAT	KN.....KT...HFSV.....RLLK..FSR..EKKAAKTL
O54913	KN.....KT...HFSV.....RLLK..FSR..EKKAAKTL
A1AA_BOVIN	KN.....KT...HFSV.....RLLK..FSR..EKKAAKTL
A1AA_CANFA	KN.....KT...HFSV.....RLLK..FSR..EKKAAKTL
A1AA_RABIT	KN.....KT...HFSV.....RLLK..FSR..EKKAAKTL
A1AA_HUMAN	KT.....KT...HFSV.....RLLK..FSR..EKKAAKTL
A1AA_ORYLA	PS.....RT...HFAI.....RLLK..FSR..EKKAAKTL
O96716	K.....EKKAAKTL
O75963	LIYGLWNKTVRKELLGMCFGDRYYREPFOVQ..RQRTSRLF
HGPRBMY8	SEDDVEAVNIPESLPPSRNSNS.NPPLPRCYQCKAAKVII

ACM4_CHICK
YDBM_CAEEL
5H1A_HUMAN
5H1A_MOUSE
5H1A_FUGRU
5HT_LYMST
A1AD_HUMAN
A1AD_MOUSE
Q13675
Q13729
O60451
A1AA_RAT
O54913
A1AA_BOVIN
A1AA_CANFA
A1AA_RABIT
A1AA_HUMAN
A1AA_ORYLA
O96716
O75963
HGPRBMY8

ACM4_CHICK
YDBM_CAEEL
5H1A_HUMAN
5H1A_MOUSE
5H1A_FUGRU
5HT_LYMST
A1AD_HUMAN
A1AD_MOUSE
Q13675
Q13729
O60451
A1AA_RAT
O54913
A1AA_BOVIN
A1AA_CANFA
A1AA_RABIT
A1AA_HUMAN
A1AA_ORYLA
O96716
O75963
HGPRBMY8

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FIG. 6I

ACM4_CHICK	~~~~~
YDBM_CAEEL	~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~~~~~
A1AD_HUMAN	EWRLLGPFRRPTTQLRAKVSSLSHKIRAGGAQRAEAACAQ
A1AD_MOUSE	EWRLLGPLQRPTTQLRAKVSSLSHKFRSGGARRAETACAL
Q13675	KRSRVTRLECS....GMILAHCN..LRLPGSRDSPASASQ
Q13729	HT.PMT~~~~~
O60451	GMDCRYFTKNC....REHIKHVN..FMMPPWRKGLEC~~~
A1AA_RAT	RSKSFLQVCCCV.GSSAPRPEEN..HQVPTIKIHTISLGE
O54913	RSKSFLQVCCCV.GSSTPRPEEN..HQVPTIKIHTISLGE
A1AA_BOVIN	RSKSFLQVCCCL.GPSTPSHGEN..HQIPTIKIHTISLSE
A1AA_CANFA	~~~~~
A1AA_RABIT	RSKSFLQVCCCV.GPSTPNPGEN..HQVPTIKIHTISLSE
A1AA_HUMAN	RSKSFLQVCCCV.GPSTPSLDKN..HQVPTIKVHTISLSE
A1AA_ORYLA	CNKSLHRTCCCILRARTPTQDPAPLGDLPPTIKIHQLSLSE
O96716	~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~
ACM4_CHICK	~~~~~
YDBM_CAEEL	~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~~~~~
A1AD_HUMAN	RSEVEAVSLGVPHEVAEGATCQAYELADYSNLRETDI~~~
A1AD_MOUSE	RSEVEAVSLNVPQDGAEAVICQAYEPGDLSNLRETDI~~~
Q13675	AAGTTGDVPPGRRHQAQLIFVFLVETGFHHVGQDDLDLLT
Q13729	~~~~~
O60451	~~~~~
A1AA_RAT	NGEEV~~~~~
O54913	NGEEV~~~~~
A1AA_BOVIN	NGEEV~~~~~
A1AA_CANFA	~~~~~
A1AA_RABIT	NGEEV~~~~~
A1AA_HUMAN	NGEEV~~~~~
A1AA_ORYLA	KGESV~~~~~
O96716	~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~

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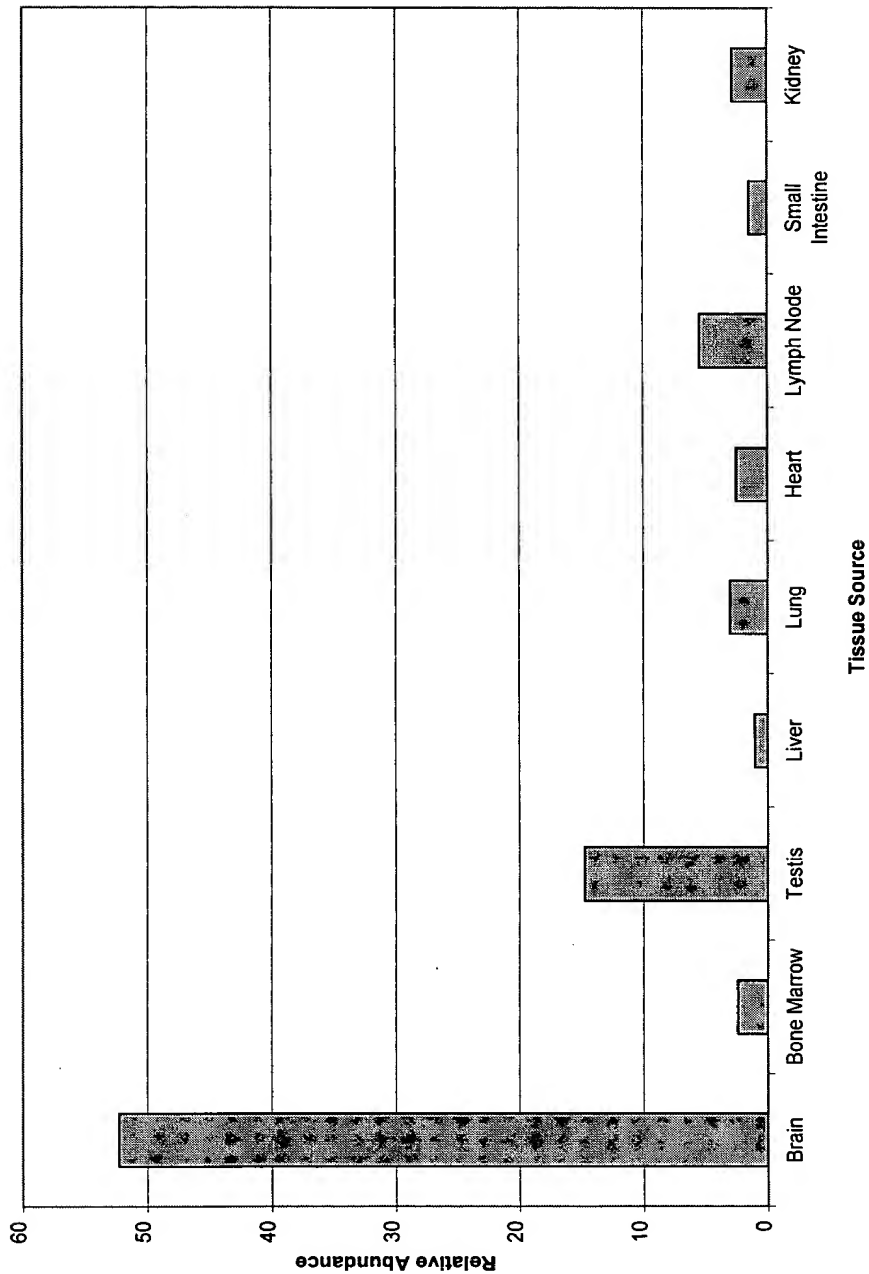
FIG. 6J

ACM4_CHICK	~
YDBM_CAEEL	~
5H1A_HUMAN	~
5H1A_MOUSE	~
5H1A_FUGRU	~
5HT_LYMST	~
A1AD_HUMAN	~
A1AD_MOUSE	~
Q13675	S
Q13729	~
O60451	~
A1AA_RAT	~
O54913	~
A1AA_BOVIN	~
A1AA_CANFA	~
A1AA_RABIT	~
A1AA_HUMAN	~
A1AA_ORYLA	~
O96716	~
O75963	~
HGPRBMY8	~

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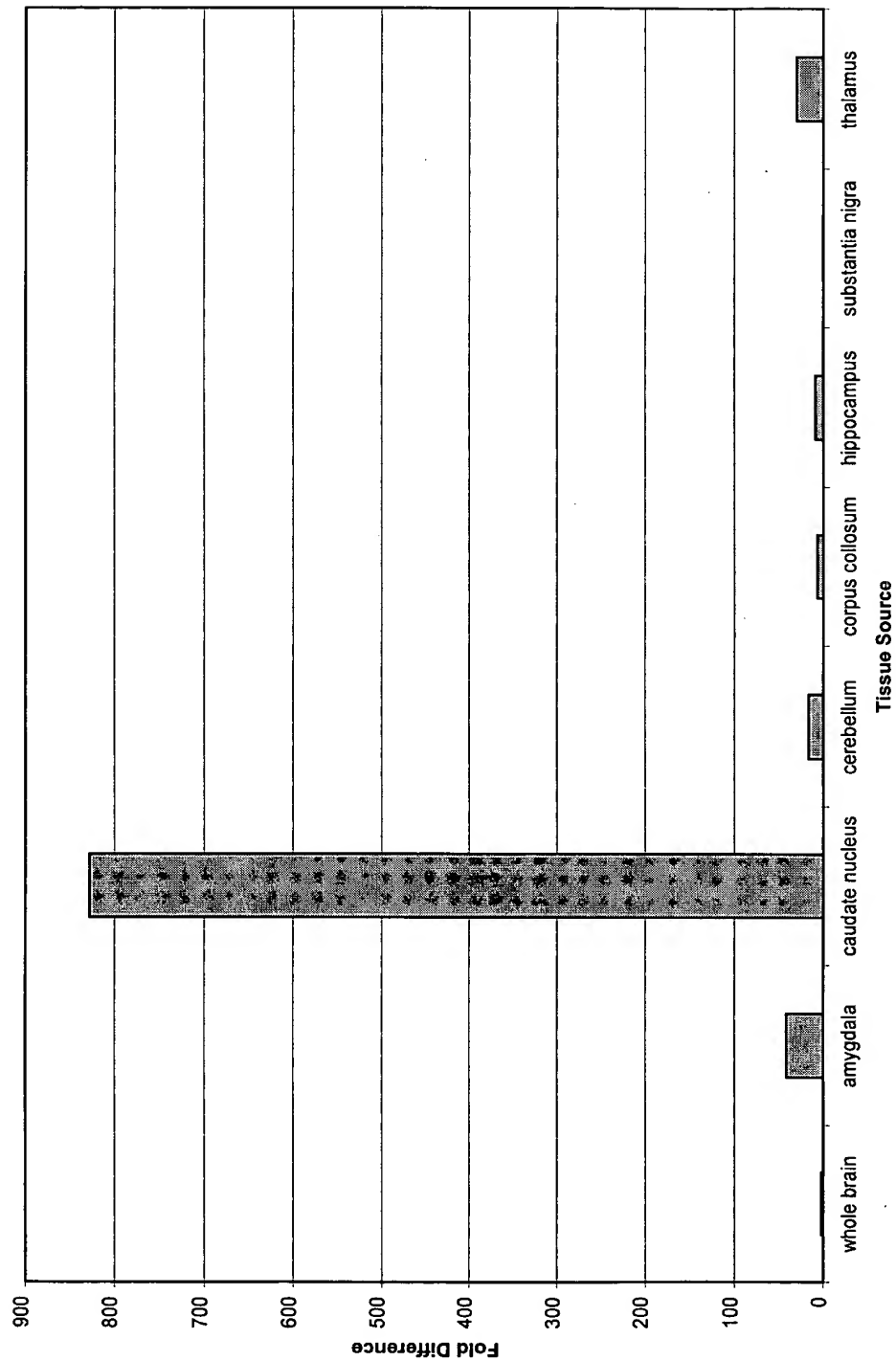
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FIG. 7



D0047 NP

FIG. 8



D0047 NP

FIG. 9

HGPRBMY8	MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
AL390879	MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
AX148250	MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
AX080495	MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
HGPRBMY8	QLLQVTNRFI FNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
AL390879	QLLQVTNRFI FNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
AX148250	QLLQVTNRFI FNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
AX080495	QLLQVTNRFI FNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
HGPRBMY8	TIVVVSVDRLYSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAADFERN
AL390879	TIVVVSVDRLYSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAADFERN
AX148250	TIVVVSVDRLYSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAADFERN
AX080495	TIVVVSVDRLYSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAADFERN
HGPRBMY8	LCSMIWGASPSYTI LSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
AL390879	LCSMIWGASPSYTI LSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
AX148250	LCSMIWGASPSYTI LSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
AX080495	LCSMIWGASPSYTI LSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
HGPRBMY8	CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGS LKAKEGSTGTSESSVEA
AL390879	CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGS LKAKEGSTGTSESSVEA
AX148250	CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGS LKAKEGSTGTSESSVEA
AX080495	CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGS LKAKEGSTGTSESSVEA
HGPRBMY8	RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
AL390879	RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
AX148250	RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
AX080495	RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
HGPRBMY8	NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS YVLSLGPYCFLAV
AL390879	NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS YVLSLGPYCFLAV
AX148250	NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS YVLSLGPYCFLAV
AX080495	NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS YVLSLGPYCFLAV
HGPRBMY8	LAVWVDVETQVPQWVITIIIWLFLLQCCIHYPVYGYMHKTIKKEIQDMLKKFFCCKEPPK
AL390879	LAVWVDVETQVPQWVITIIIWLFLLQCCIHYPVYGYMHKTIKKEIQDMLKKFFCCKEPPK
AX148250	LAVWVDVETQVPQWVITIIIWLFLLQCCIHYPVYGYMHKTIKKEIQDMLKKFFCCKEPPK
AX080495	LAVWVDVETQVPQWVITIIIWLFLLQCCIHYPVYGYMHKTIKKEIQDMLKKFFCCKEPPK
HGPRBMY8	EDSHPDLPGTEGGTEGKIVPSYDSATFP~
AL390879	EDSHPDLPGTEGGTEGKIVPSYDSATFP*
AX148250	EDSHPDLPGTEGGTEGKIVPSYDSATFP*
AX080495	EDSHPDLPGTEGGTEGKIVPSYDSATFP*

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FIG. 10A

AX080495 GCCTGCAACCTGTCTCACGCCCCTCTGGCTGTTGCCATGACGTCCACCTGC
HGPRBMY8 ~~~GCAACCTGTCTCACGCCCCTCTGGCTGTTGCCATGACGTCCACCTGC
AL390879 ~~~~~~ATGACGTCCACCTGC
AX148250 ~~~~~~ATGACGTCCACCTGC

AX080495 ACCAACAGCAGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCTCTC
HGPRBMY8 ACCAACAGCAGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCTCTC
AL390879 ACCAACAGCAGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCTCTC
AX148250 ACCAACAGCAGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCTCTC

AX080495 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG
HGPRBMY8 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG
AL390879 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG
AX148250 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG

AX080495 TTATCTTCCTCGCCGCTCTTTTCGTCGGCAACATAGTGCTGGCGCTAGTG
HGPRBMY8 TTATCTTCCTCGCCGCTCTTTTCGTCGGCAACATAGTGCTGGCGCTAGTG
AL390879 TTATCTTCCTCGCCGCTCTTTTCGTCGGCAACATAGTGCTGGCGCTAGTG
AX148250 TTATCTTCCTCGCCGCTCTTTTCGTCGGCAACATAGTGCTGGCGCTAGTG

AX080495 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
HGPRBMY8 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
AL390879 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
AX148250 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA

AX080495 CCTCCTCGTCACCGACCTGCTGCAGATTTTCGCTCGTGGCCCCCTGGGTGG
HGPRBMY8 CCTCCTCGTCACCGACCTGCTGCAGATTTTCGCTCGTGGCCCCCTGGGTGG
AL390879 CCTCCTCGTCACCGACCTGCTGCAGATTTTCGCTCGTGGCCCCCTGGGTGG
AX148250 CCTCCTCGTCACCGACCTGCTGCAGATTTTCGCTCGTGGCCCCCTGGGTGG

AX080495 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG
HGPRBMY8 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG
AL390879 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG
AX148250 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG

AX080495 GCCCTGGTTAGCCTCACCCACCTGTTGCCTTCGCCAGCGTCAACACCAT
HGPRBMY8 GCCCTGGTTAGCCTCACCCACCTGTTGCCTTCGCCAGCGTCAACACCAT
AL390879 GCCCTGGTTAGCCTCACCCACCTGTTGCCTTCGCCAGCGTCAACACCAT
AX148250 GCCCTGGTTAGCCTCACCCACCTGTTGCCTTCGCCAGCGTCAACACCAT

AX080495 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
HGPRBMY8 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
AL390879 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
AX148250 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT

AX080495 ACCCGTCCAAGATGACCCAGCGCCGCGTTACCTGCTCCTCTATGGCACC
HGPRBMY8 ACCCGTCCAAGATGACCCAGCGCCGCGTTACCTGCTCCTCTATGGCACC
AL390879 ACCCGTCCAAGATGACCCAGCGCCGCGTTACCTGCTCCTCTATGGCACC
AX148250 ACCCGTCCAAGATGACCCAGCGCCGCGTTACCTGCTCCTCTATGGCACC

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FIG. 10B

AX080495	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
HGPRBMY8	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AL390879	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AX148250	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AX080495	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
HGPRBMY8	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AL390879	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AX148250	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AX080495	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
HGPRBMY8	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AL390879	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AX148250	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AX080495	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
HGPRBMY8	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
AL390879	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
AX148250	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
AX080495	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA
HGPRBMY8	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA
AL390879	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA
AX148250	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA
AX080495	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
HGPRBMY8	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AL390879	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AX148250	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AX080495	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
HGPRBMY8	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AL390879	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AX148250	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AX080495	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
HGPRBMY8	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AL390879	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AX148250	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AX080495	GAAGCACGGGGACCACTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
HGPRBMY8	GAAGCACGGGGACCACTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AL390879	GAAGCACGGGGACCACTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AX148250	GAAGCACGGGGACCACTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AX080495	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
HGPRBMY8	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
AL390879	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
AX148250	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA

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FIG. 10C

AX080495	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
HGPRBMY8	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AL390879	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AX148250	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AX080495	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGCGCATGGAGTTT
HGPRBMY8	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AL390879	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AX148250	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AX080495	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
HGPRBMY8	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
AL390879	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
AX148250	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
AX080495	CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCTCCTC
HGPRBMY8	CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCTCCTC
AL390879	CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCTCCTC
AX148250	CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCTCCTC
AX080495	TGCCCAGGTGCTACCAAGTGCAGCATTGCTAAAGTGATCTTCATCATCATT
HGPRBMY8	TGCCCAGGTGCTACCAAGTGCAGCATTGCTAAAGTGATCTTCATCATCATT
AL390879	TGCCCAGGTGCTACCAAGTGCAGCATTGCTAAAGTGATCTTCATCATCATT
AX148250	TGCCCAGGTGCTACCAAGTGCAGCATTGCTAAAGTGATCTTCATCATCATT
AX080495	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTCCTGGC
HGPRBMY8	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTCCTGGC
AL390879	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTCCTGGC
AX148250	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTCCTGGC
AX080495	CGTGTGGGTGGATGTGCGAAACCCAGGTACCCAGTGGGTGATCACCATAA
HGPRBMY8	CGTGTGGGTGGATGTGCGAAACCCAGGTACCCAGTGGGTGATCACCATAA
AL390879	CGTGTGGGTGGATGTGCGAAACCCAGGTACCCAGTGGGTGATCACCATAA
AX148250	CGTGTGGGTGGATGTGCGAAACCCAGGTACCCAGTGGGTGATCACCATAA
AX080495	TCATCTGGCTTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
HGPRBMY8	TCATCTGGCTTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AL390879	TCATCTGGCTTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AX148250	TCATCTGGCTTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AX080495	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
HGPRBMY8	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AL390879	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AX148250	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AX080495	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCCG
HGPRBMY8	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCCG
AL390879	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCCG
AX148250	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCCG

	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	

FIG. 10D

AX080495	GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT
HGPRBMY8	GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT
AL390879	GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT
AX148250	GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT

AX080495 ACTTTTCCTTGAAGTTAGTTCTAAGGCAAACCTTGAAAATCAGTCCTTCA
HGPRBM8 ACTTTTCCTTGAAGTTAGTTCTAAGGCAAACCTT~~~~~
AL390879 ACTTTTCCTTGA~~~~~
AX148250 ACTTTTCCTTGA~~~~~

AX080495 GCCACAGCTATTTAGAGCTTTAAAACTACCAGGTTCAATCACTGGTTATG
HGPRBMY8 ~~~~~
AL390879 ~~~~~
AX148250 ~~~~~

```
AX080495  CTTTCTGTG
HGPRBMY8  ~~~~~
AL390879  ~~~~~
AX148250  ~~~~~
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FIG. 11

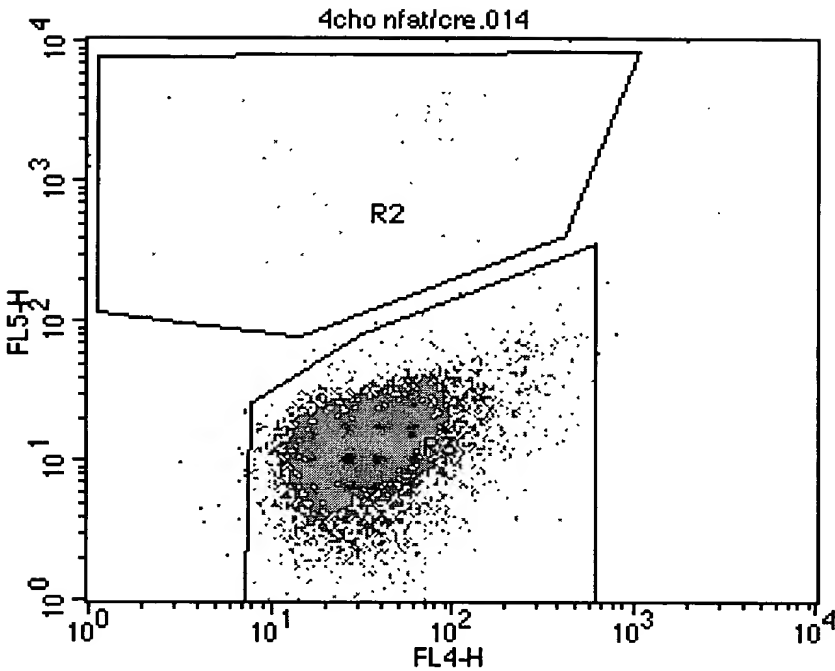


FIG. 12

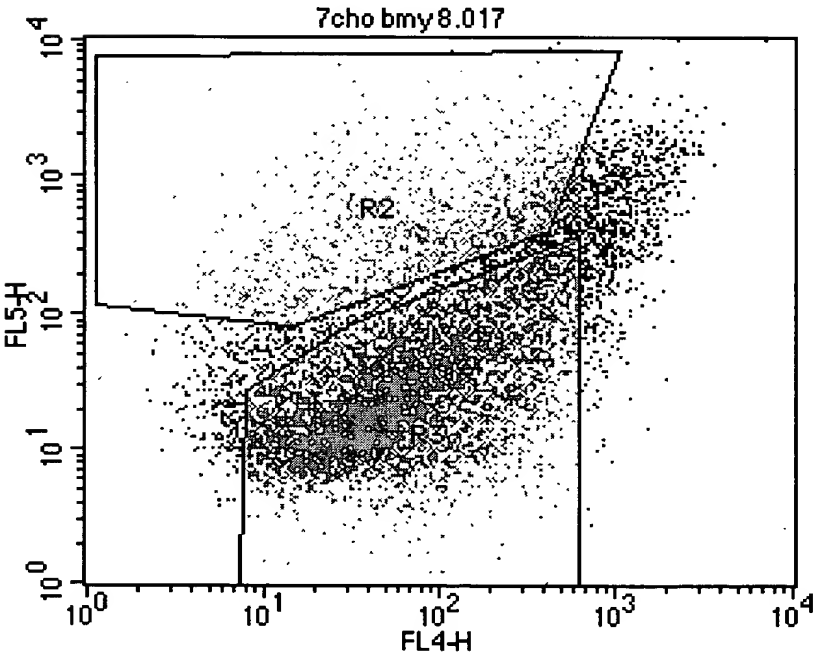


FIG. 13

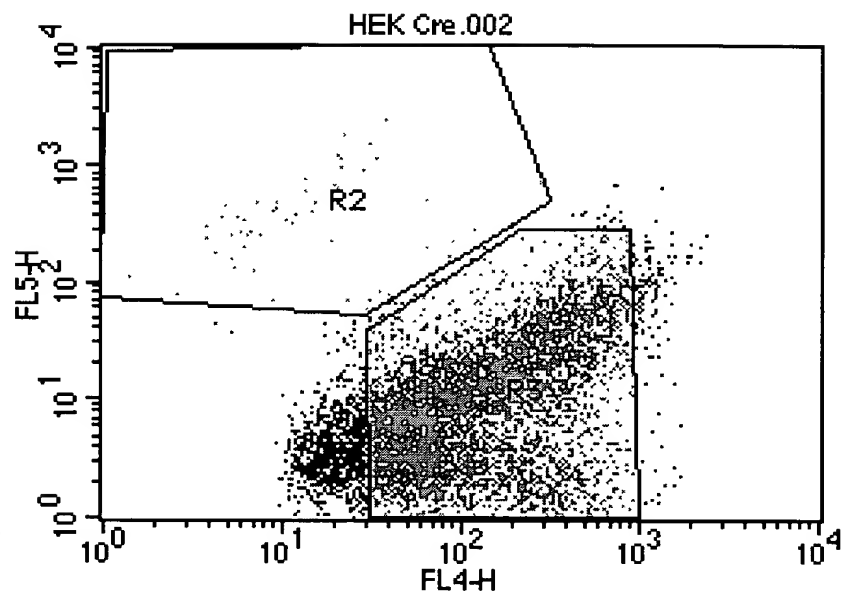


FIG. 14

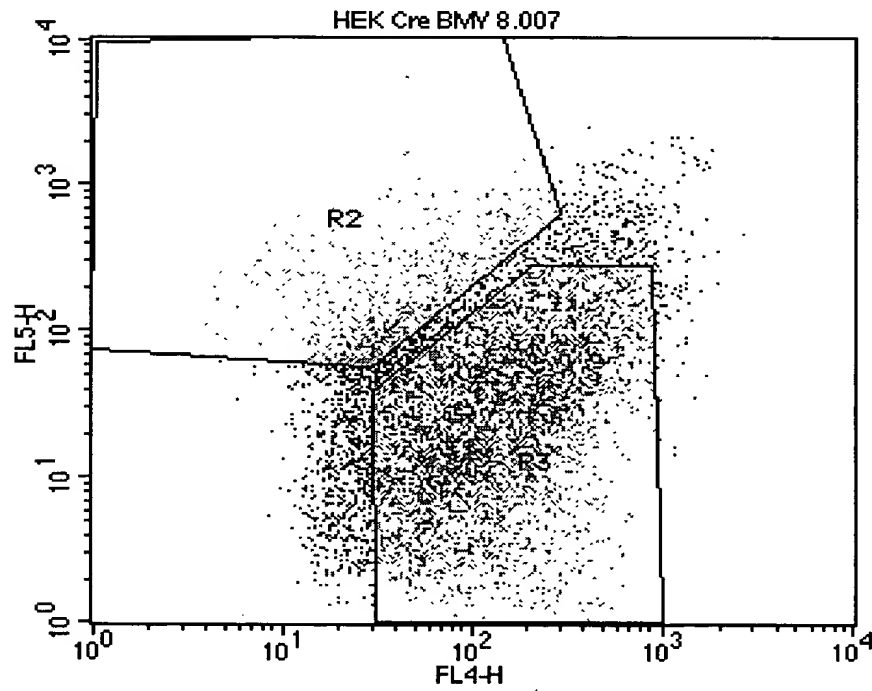
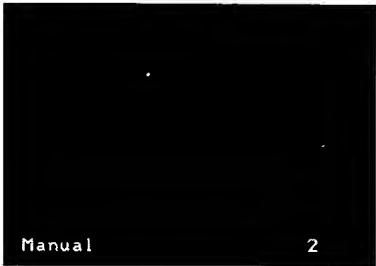
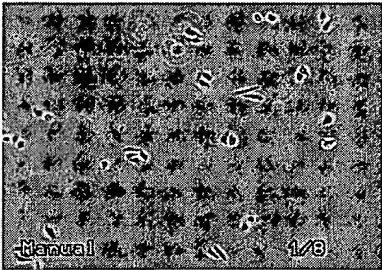
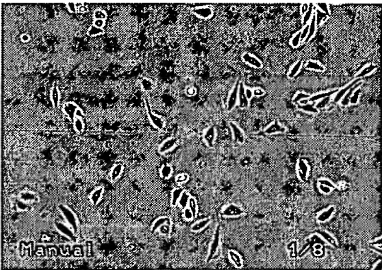


FIG. 15

a. CHO-NFAT G alpha 15 (Fluorescent vs. Bright Field)



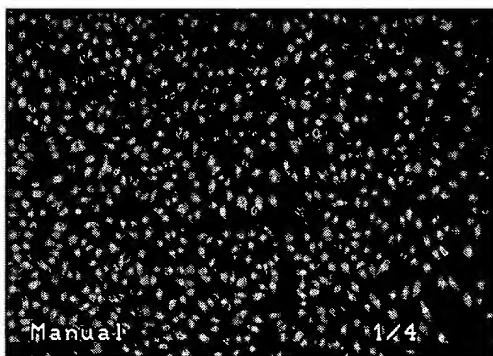
b. CHO-NFAT/ G alpha 15 HGPRBMY8 (Fluorescent vs. Bright Field)



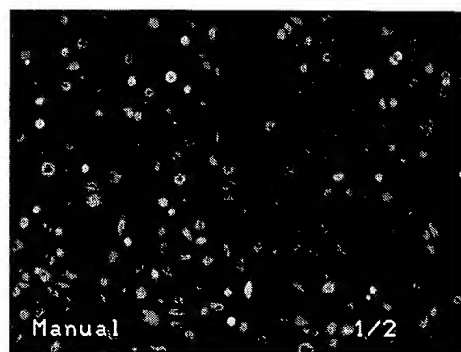
D0047 NP

FIG. 16

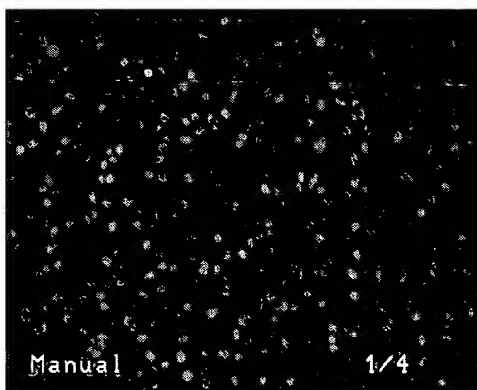
a. CHO-NFAT/CRE



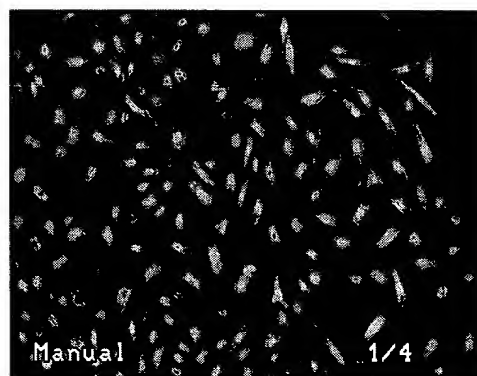
b. CHO-NFAT/CRE + F/T/P



c. CHO-NFAT/CRE oGPCR-Intermediate

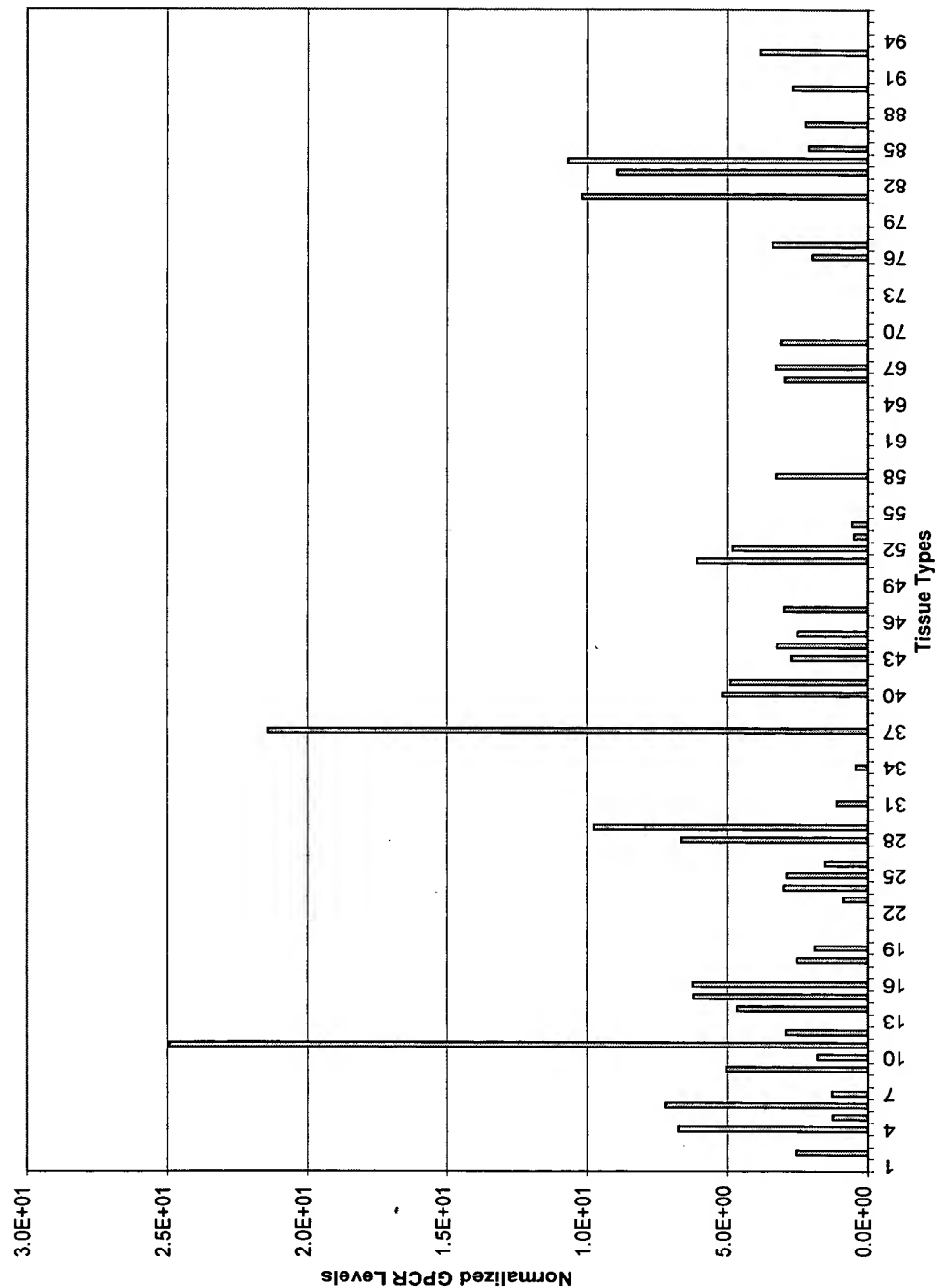


d. CHO-NFAT/CRE oGPCR high



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FIG. 17



Time	Temperature	Pressure	Humidity	Wind	Clouds	Visibility	Remarks
0000	10.0	1013.2	85	0.0	0.0	10.0	Clear
0100	10.0	1013.2	85	0.0	0.0	10.0	Clear
0200	10.0	1013.2	85	0.0	0.0	10.0	Clear
0300	10.0	1013.2	85	0.0	0.0	10.0	Clear
0400	10.0	1013.2	85	0.0	0.0	10.0	Clear
0500	10.0	1013.2	85	0.0	0.0	10.0	Clear
0600	10.0	1013.2	85	0.0	0.0	10.0	Clear
0700	10.0	1013.2	85	0.0	0.0	10.0	Clear
0800	10.0	1013.2	85	0.0	0.0	10.0	Clear
0900	10.0	1013.2	85	0.0	0.0	10.0	Clear
1000	10.0	1013.2	85	0.0	0.0	10.0	Clear
1100	10.0	1013.2	85	0.0	0.0	10.0	Clear
1200	10.0	1013.2	85	0.0	0.0	10.0	Clear
1300	10.0	1013.2	85	0.0	0.0	10.0	Clear
1400	10.0	1013.2	85	0.0	0.0	10.0	Clear
1500	10.0	1013.2	85	0.0	0.0	10.0	Clear
1600	10.0	1013.2	85	0.0	0.0	10.0	Clear
1700	10.0	1013.2	85	0.0	0.0	10.0	Clear
1800	10.0	1013.2	85	0.0	0.0	10.0	Clear
1900	10.0	1013.2	85	0.0	0.0	10.0	Clear
2000	10.0	1013.2	85	0.0	0.0	10.0	Clear
2100	10.0	1013.2	85	0.0	0.0	10.0	Clear
2200	10.0	1013.2	85	0.0	0.0	10.0	Clear
2300	10.0	1013.2	85	0.0	0.0	10.0	Clear
2400	10.0	1013.2	85	0.0	0.0	10.0	Clear

FIG. 18A

1	ATGACGTCACCACTGCAACACAGCACGCGAGAGTAACAGCAGCCACACGTCATGGCC	60
1	M T S T C T N S T R E S N S S H T C M P	20
61	CTCTCCAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGGTTATC	120
21	L S K M P I S L A H G I I R S T V L V I	40
121	TTCCTCGCCGCTCTTTTCGTGCGCAACATAGTGCTGGCGCTAGTGTTGCAGCGCAAGCCG	180
41	F L A A S F V G N I V L A L V L Q R K P	60
181	CAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAACCTCCTCGTCACCGACCTGCTGCAG	240
61	Q L L Q V T N R F I F N L L V T D L L Q	80
241	ATTTGCTCGTGGCCCCCTGGGTGGTGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAAC	300
81	I S L V A P W V V A T S V P L F W P L N	100
301	AGCCACTTCTGCACGGCCCTGGTTAGCCTCACCCACCTGTTGCGCTTCGCCAGCGTCAAC	360
101	S H F C T A L V S L T H L F A F A S V N	120
361	ACCATTGTCTGGTGTCTAGTGGATCGCTACTTGTCCATCATCCACCTCTCTCCTACCCG	420
121	T I V X V S V D R Y L S I I H P L S Y P	140
421	TCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACCTGGATTGTGGCCATC	480
141	S K M T Q R R G Y L L L Y G T W I V A I	160
481	CTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCAGGCTGCCTTTGATGAGCGCAATGCT	540
161	L Q S T P P L Y G W G Q A A F D E R N A	180
541	CTCTGCTCCATGATCTGGGGGGCCAGCCCCAGCTACACTATTCTCAGCGTGGTGTCTTC	600
181	L C S M I W G A S P S Y T I L S V V S F	200
601	ATCGTCATTCCACTGATTGTCTATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGG	660
201	I V I P L I V M I A C Y S V V F C A A R	220
661	AGGCAGCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCGAGTCAAGGAC	720
221	R Q H A L L Y N V K R H S L E V R V K D	240
721	TGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAGTTCCAGGATGAGAGT	780
241	C V E N E D E E G A E K K E E F Q D E S	260
781	GAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGCCAAGGAGGGCAGAATGGAAGCCAAG	840
261	E F R R Q H E G E V K A K E G R M E A K	280
841	GACGGCAGCCTGAAGGCCAAGGAAGGAAGCACGGGGACCAAGTGAAGTGTAGAGGCC	900
281	D G S L K A K E G S T G T S E S S V E A	300

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FIG. 18B

901 AGGGGCAGCGAGGAGGTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGT 960
301 R G S E E V R E S S T V A S D G S M E G 320

961 AAGGAAGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCACAGAG 1020
321 K E G S T K V E E N S M K A D K G R T E 340

1021 GTCAACCAGTGCAGCATTGACTTGGGTGAAGATGNCATGGAGTTTGGTGAAGACGACATC 1080
341 V N Q C S I D L G E D X M E F G E D D I 360

1081 AATTTCAAGTGAAGTACGTCGAGGAGTGAACATCCCGAGAGCCTCCACCCAGTCGT 1140
361 N F S E D D V E A V N I P E S L P P S R 380

1141 CGTAACAGCAACAGCAACCCTCCTCTGCCCAGGTGCTACCAGTGCAAAGCTNNNAAAGTG 1200
381 R N S N S N P P L P R C Y Q C K A X K V 400

1201 ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTCTAGCAGTC 1260
401 I F I I I F S Y V L S L G P Y C F L A V 420

1261 CTGGCCGTGTGGGTGGATGTGAAACCCAGGTACCCAGTGGGTGATCACCATAATCATC 1320
421 L A V W V D V E T Q V P Q W V I T I I I 440

1321 TGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGCTACATGCACAAGACC 1380
441 W L F F L Q C C I H P Y V Y G Y M H K T 460

1381 ATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTTCTTCTGCAAGGAAAAGCCCCGAAA 1440
461 I K K E I Q D M L K K F F C K E K P P K 480

1441 GAAGATAGCCACCCAGACCTGCCCAGAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCT 1500
481 E D S H P D L P G T E G G T E G K I V P 500

1501 TCCTACGATTCTGCTACTTTTCCTTGA 1527
501 S Y D S A T F P 508

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